

GenCore version 5.1.4.p5.1578  
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OM protein - protein search, using sv model

Run on: April 23, 2003, 11:01:50 ; Search time 39 seconds  
2217.427 Million cell updates/sec

Title: US-10-004-551-6

Perfect score: 3400 1 MISAANSITGKIGLFLQ.....SSNSNFUSGIPDSUSHS 649

Sequence:

Scoring table: HMM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seps, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: A\_Geneseq\_101002.\*  
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10: /SID52/cgqdata/geneseq/emb1/AA1988.DAT.\*  
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22: /SID52/cgqdata/geneseq/emb1/AA2000.DAT.\*  
23: /SID52/cgqdata/geneseq/emb1/AA2001.DAT.\*  
24: /SID52/cgqdata/geneseq/emb1/AA2002.DAT.\*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and as derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3400	100.0	649	22	AAU73215
2	3400	100.0	649	22	AAU73215
3	3400	100.0	649	22	AAU73215
4	3400	100.0	649	22	AAU73215
5	3400	100.0	649	22	AAU73215
6	3396	99.9	649	22	AAU73215
7	3395	99.9	649	22	AAU73215
8	3395	99.9	649	22	AAU73215
9	3395	99.9	649	22	AAU73215
10	3284	96.6	649	22	AAU73215

11	3284	96.6	649	22	AAU73215
12	3274	96.3	623	23	AAU73215
13	3274	96.3	623	23	AAU73215
14	3269	96.1	623	23	AAU73215
15	3269	96.1	623	23	AAU73215
16	3210	94.4	613	22	AAU73215
17	2925.5	93.1	592	22	AAU73215
18	2925.5	93.1	592	22	AAU73215
19	2925.5	93.1	592	22	AAU73215
20	1944	87.2	372	22	AAU73215
21	1944	87.2	372	22	AAU73215
22	1944	87.2	372	22	AAU73215
23	1944	87.2	372	22	AAU73215
24	1944	87.2	372	22	AAU73215
25	1866.5	84.9	664	23	AAU73215
26	1866.5	84.9	664	23	AAU73215
27	1866.5	84.9	664	23	AAU73215
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31	1866.5	84.9	664	23	AAU73215
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33	576	19.9	312	22	AAU73215
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36	546	16.1	110	22	AAU73215
37	398.7	11.7	705	22	AAU73215
38	398.7	11.7	705	22	AAU73215
39	397	11.7	705	22	AAU73215
40	397	11.7	705	22	AAU73215
41	397	11.7	705	22	AAU73215
42	397	11.7	705	22	AAU73215
43	397	11.7	705	22	AAU73215
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## ALIGNMENTS

RESULT 1  
AAU73215  
ID AAU73215 standard; Protein: 649 AA.  
AC AAU73215;  
DT 18-DEC-2001 (first entry)  
XX HUMAN PRO polypeptide sequence #192.  
XX HUMAN PRO polypeptide sequence #192.  
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNP-alpha;  
KW human; human; human; human; human; human; human; human; human;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX Homo sapiens.  
XX NC20016848-A2.  
XX 20-SEP-2001.  
XX 28-FEB-2001, 2000NC-U060620.  
XX 01-MAR-2000, 2000NC-T095601.  
XX 02-MAR-2000, 2000NC-T095601.  
XX 03-MAR-2000, 2000NC-T095601.  
XX 04-MAR-2000, 2000NC-186686P.  
XX 05-MAR-2000, 2000NC-186686P.  
XX 06-MAR-2000, 2000NC-186686P.  
XX 07-MAR-2000, 2000NC-186686P.  
XX 08-MAR-2000, 2000NC-186686P.  
XX 09-MAR-2000, 2000NC-186686P.  
XX 10-MAR-2000, 2000NC-186686P.  
XX 11-MAR-2000, 2000NC-186686P.  
XX 12-MAR-2000, 2000NC-186686P.  
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XX 14-MAR-2000, 2000NC-186686P.  
XX 15-MAR-2000, 2000NC-186686P.  
XX 16-MAR-2000, 2000NC-186686P.  
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XX 18-MAR-2000, 2000NC-186686P.  
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XX 21-MAR-2000, 2000NC-186686P.  
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XX 23-MAR-2000, 2000NC-186686P.  
XX 24-MAR-2000, 2000NC-186686P.  
XX 25-MAR-2000, 2000NC-186686P.  
XX 26-MAR-2000, 2000NC-186686P.  
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XX 28-MAR-2000, 2000NC-186686P.  
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XX 34-MAR-2000, 2000NC-186686P.  
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XX 42-MAR-2000, 2000NC-186686P.  
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XX 44-MAR-2000, 2000NC-186686P.  
XX 45-MAR-2000, 2000NC-186686P.

[illegible]

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(GUTH) GENETECH INC.

PA Batson DK, Filveroff E, Gerritsen DE, Goddard A, Godowski PJ;  
 PI Grissold CJ, Gurney AJ, Watanabe CK, Wood WT;  
 XX NFWI, 2001-183260/18.  
 DR NFWI, 2001-183260/18.  
 DR NFWI, 2001-183260/18.  
 DR NFWI, 2001-183260/18.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
 PT molecular biology, including use as hybridization probes, and in  
 PT chromosome and gene mapping.  
 PS Claim 12, Fig 132; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and  
 CC anti-PRO antibodies are useful for preparation of a medicament useful  
 CC in the treatment of a condition which is responsive to the PRO protein,  
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
 CC used in the treatment of a condition which is responsive to the PRO  
 CC coding sequence has applications in molecular biology, including use as  
 CC hybridization probes, and in chromosome and gene mapping.

Sequence 649 AA;

Query Match 100.0%; Score 3400; DB 22; Length 649;  
 Best Local Similarity 100.0%; Pred No. 7, 5e+20;  
 Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISANSTLTGKIGLQVAVSWANSCVPCDCAGTICNDRYSITFCIPEDA 60  
 DB 1 MISANSTLTGKIGLQVAVSWANSCVPCDCAGTICNDRYSITFCIPEDA 60  
 QY 61 TLTALANNQINAGIPEDLANLAVERTLVNLSDEFFPAKYEALQNNRTIT 120  
 DB 61 TLTALANNQINAGIPEDLANLAVERTLVNLSDEFFPAKYEALQNNRTIT 120  
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 DB 121 YNSLSTPTLEEHLNDNSNYSNTGCAVSGKYLRTLSNRLSTPGLPTTEL 180  
 QY 181 RLDNNESTTSSPGLQSLSEKLVLLQGLLANNGLGQVNFVLLFTELAVYNSEDA 240  
 DB 181 RLDNNESTTSSPGLQSLSEKLVLLQGLLANNGLGQVNFVLLFTELAVYNSEDA 240  
 QY 241 PNLPTNTEHLVLAQNNVETPRVYGLQITLNDNSNLSLPGCTFDLNTQI 300  
 DB 241 PNLPTNTEHLVLAQNNVETPRVYGLQITLNDNSNLSLPGCTFDLNTQI 300  
 QY 301 ILNNPTQCCQKMYVWMLQSLPVVWVGLQKQAPKRYGVALYDLNLPCCDSII 360  
 DB 301 ILNNPTQCCQKMYVWMLQSLPVVWVGLQKQAPKRYGVALYDLNLPCCDSII 360  
 QY 361 VSTQITLTATNTPVPAQGPVAPVQPDQKMPKLDQDQGTGSKRTITVNSVTS 420  
 DB 361 VSTQITLTATNTPVPAQGPVAPVQPDQKMPKLDQDQGTGSKRTITVNSVTS 420  
 QY 421 DTIHSKRLAFLWALSHKLSHGFARSITETIVGSRHSITVVALSPGPKVCH 480  
 DB 421 DTIHSKRLAFLWALSHKLSHGFARSITETIVGSRHSITVVALSPGPKVCH 480  
 QY 481 PMSKSLHFLPFTVCTETAEALNFWPTTLNDEKFTNPNFLAALTGAVALL 540  
 DB 481 PMSKSLHFLPFTVCTETAEALNFWPTTLNDEKFTNPNFLAALTGAVALL 540  
 QY 541 TALLAALCWNVHNSGISPSKNSKSKDQAPAGTKONSLIDETISQMLPTS 600  
 DB 541 TALLAALCWNVHNSGISPSKNSKSKDQAPAGTKONSLIDETISQMLPTS 600  
 QY 601 NFETICEEVEVETIFFPNNGLNKNHSSSSSSSSSSSSSSSSSSSSSSSSSS 649  
 DB 601 NFETICEEVEVETIFFPNNGLNKNHSSSSSSSSSSSSSSSSSSSSSSSSSS 649

RESULT 3

AA870533

ID AA870533 standard; Protein; 649 AA.

AC AA870533;

XX 09-MAR-2001 (first entry)

UT

XX

XX Human PRO3 protein sequence SEQ ID NO:6.

XX

XX Human PRO3, cytotretic; immunomodulatory; reproduction

XX immune associated disorder; gestational disease; pre-eclampsia;

XX chromosome 30.

XX homo sapiens.

XX W0200110902.A2.

XX 15-FEB-2001.

XX 11-AUG-2000; 2000MO-U021857.

XX 11-AUG-1999; 590US-0148433.

XX 11-AUG-2000; 2000US-0148433.

XX (CITER-) CITRAGEN CORP.

XX Shinketsu RA, Fernandes R;

XX NFWI: 2001-147509/15.

XX NFWI: AA874434.

XX Nucleic acids encoding secreted polypeptides, designated PRO3

XX polypeptides, useful for treating a syndrome associated with a

XX PRO3-associated disorder, e.g. cancer.

XX Claim 1; Page 13-15; 16pp; English.

XX The present invention describes isolated nucleic acids encoding secreted  
 CC polypeptides, designated PRO3 polypeptides (i.e. a PRO polypeptide where  
 CC the amino acid sequence is identical to that of the PRO protein), and  
 CC immunomodulatory and reproduction activities, and can be used in gene  
 CC therapy, and as PRO3 antagonists and PRO3 agonists. PRO3 polypeptides,  
 CC and as PRO3 antagonists and PRO3 agonists, and as PRO3 agonists, are  
 CC medicament for treating a syndrome associated with a PRO3-associated  
 CC disorder, e.g. a cell proliferation and/or differentiation disorder  
 CC (e.g. cancer or immune associated disorders) and a gestational disease  
 CC (e.g. pre-eclampsia). The PRO3 polypeptides are also useful for the  
 CC activity or of interest or predisposition to a PRO3-associated disorder.  
 CC AA874432 to AA874448 encode the specifically claimed human PRO3  
 CC polypeptides PRO3 to PRO37 given in AA870531 to AA870547.

Sequence 649 AA;

Query Match 100.0%; Score 3400; DB 22; Length 649;  
 Best Local Similarity 100.0%; Pred No. 7, 5e+20;  
 Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISANSTLTGKIGLQVAVSWANSCVPCDCAGTICNDRYSITFCIPEDA 60  
 DB 1 MISANSTLTGKIGLQVAVSWANSCVPCDCAGTICNDRYSITFCIPEDA 60  
 QY 61 TLTALANNQINAGIPEDLANLAVERTLVNLSDEFFPAKYEALQNNRTIT 120  
 DB 61 TLTALANNQINAGIPEDLANLAVERTLVNLSDEFFPAKYEALQNNRTIT 120  
 QY 121 YNSLSTPTLEEHLNDNSNYSNTGCAVSGKYLRTLSNRLSTPGLPTTEL 180  
 DB 121 YNSLSTPTLEEHLNDNSNYSNTGCAVSGKYLRTLSNRLSTPGLPTTEL 180  
 QY 181 RLDNNESTTSSPGLQSLSEKLVLLQGLLANNGLGQVNFVLLFTELAVYNSEDA 240  
 DB 181 RLDNNESTTSSPGLQSLSEKLVLLQGLLANNGLGQVNFVLLFTELAVYNSEDA 240







601 NEPISEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 649  
 RESULT 7  
 ID AMN78907 standard; Protein: 649 AA.  
 XX AMN78907;  
 XX AMN78907;  
 XX 06-NOV-2001 (first entry)  
 XX Human protein SEQ ID NO 1569.  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
 KW hematopoietic stem cell growth factor; leukemia;  
 KW nervous system disorder; arthritis; inflammation.  
 XX Homo sapiens.  
 XX W0200157130-A2.  
 XX 09-MAY-2001.  
 XX 05-FEB-2001; 2001MO-0504098.  
 XX 09-FEB-2000; 2000US-0466374.  
 XX 27-APR-2000; 2000US-0568075.  
 XX 20-JUN-2000; 2000US-0598075.  
 XX 09-JUL-2000; 2000US-0629325.  
 XX 15-SEP-2000; 2000US-0663561.  
 XX 20-OCT-2000; 2000US-0693325.  
 XX 30-MAY-2000; 2000US-0748422.  
 XX (H582) HYSGO INC.  
 XX Tsai YT, Lin C, Dhanasek PT, Jamsat V, Zhou P, Xu C, Cao Y, Ma Y;  
 PI Zhao OA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang SM;  
 PI Xue AJ, Yang Y, Wehlman T, Goodrich R;  
 DR NPI: 2003-076383/61.  
 DR N-PSB; AA52840.  
 XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 XX useful in diagnosis and gene therapy.  
 XX Claim 20: Page 3899-3896; 6221PP: English.  
 XX The invention relates to polynucleotides (AA5145-AA53435) and the  
 XX encoded polypeptides (AA78213-AA80302) that exhibit activity elating to  
 XX cytokine, cell proliferation or cell differentiation or which may induce  
 XX cell growth. The polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 XX peptide therapy. The polypeptides have various cytokine-like activities,  
 XX e.g. stem cell growth factor activity, hematopoiesis regulating  
 XX activity, cell growth factor activity, cell differentiation activity and  
 XX activin/inhibin activity and may be useful in the diagnosis and/or  
 XX treatment of cancer, leukemia, nervous system disorders, arthritis and  
 XX inflammation.  
 XX (AA860020) are omitted as the relevant pages from the sequence listing  
 XX were missing at the time of publication.  
 XX Sequences 649 AA.  
 Query match 99.94; Score 3395; DB 22; Length 649;  
 Match 649; Identity 99.94; Positives 649;  
 Matches 649; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MISAANSTLTGKIGLQVALSNVMAKSCFVCDCMGFTCDMDRTSPICPDPA 60  
 DB 1 MISAANSTLTGKIGLQVALSNVMAKSCFVCDCMGFTCDMDRTSPICPDPA 60

61 TLTQNNQINRGTETANLAVERTLITNLSDEFFNPNLYVKELEGRNRTIT 120  
 Db 61 TLTQNNQINRGTETANLAVERTLITNLSDEFFNPNLYVKELEGRNRTIT 120  
 QY 121 YDSKSLPTLEELHDSNYSVTEGAPNSWYELPLSNHLSSTPGWLPRTIEE 180  
 Db 121 YDSKSLPTLEELHDSNYSVTEGAPNSWYELPLSNHLSSTPGWLPRTIEE 180  
 QY 181 EUDNRSTLSSPQLQSLSLKLDLNNLNNLGGDVFNVNLTSLVSNLTAA 240  
 Db 181 EUDNRSTLSSPQLQSLSLKLDLNNLNNLGGDVFNVNLTSLVSNLTAA 240  
 QY 241 PVLGSPENKSLQDNHNPVNPASSTLQLTUDNNNGNSLPGHFDLMDIOL 300  
 Db 241 PVLGSPENKSLQDNHNPVNPASSTLQLTUDNNNGNSLPGHFDLMDIOL 300  
 QY 301 PVLGSPENKSLQDNHNPVNPASSTLQLTUDNNNGNSLPGHFDLMDIOL 360  
 Db 301 PVLGSPENKSLQDNHNPVNPASSTLQLTUDNNNGNSLPGHFDLMDIOL 360  
 QY 361 TERNPCTCKMKNVWGLQSLPVYVYVGLKQVFNMGATDANLAFPCUSGI 420  
 Db 361 TERNPCTCKMKNVWGLQSLPVYVYVGLKQVFNMGATDANLAFPCUSGI 420  
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 Db 421 VSIQITTAIPNYPAGQWAPYTPQDKNPLTKQQTGSSRRTITIVSVTS 480  
 QY 481 DTHESKALPALSGLAGSPASGTETVTSRSESLVAFLESPYVQV 540  
 Db 481 DTHESKALPALSGLAGSPASGTETVTSRSESLVAFLESPYVQV 540  
 QY 541 PMETNLSLDEHPFCEETAFPMKNTTIAHREDEPCKNPLALIGQVALV 600  
 Db 541 PMETNLSLDEHPFCEETAFPMKNTTIAHREDEPCKNPLALIGQVALV 600  
 QY 601 TALLALVYVTHNSLSPSEKNSGRRCDTANRGTCKNSLREHRSFQPLIS 660  
 Db 601 TALLALVYVTHNSLSPSEKNSGRRCDTANRGTCKNSLREHRSFQPLIS 660  
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 Db 661 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 720  
 QY 721 TALLALVYVTHNSLSPSEKNSGRRCDTANRGTCKNSLREHRSFQPLIS 780  
 Db 721 TALLALVYVTHNSLSPSEKNSGRRCDTANRGTCKNSLREHRSFQPLIS 780  
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 Db 781 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 840  
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 Db 841 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 900  
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 Db 901 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 960  
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 Db 1201 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 1260  
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 QY 7921 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 7980  
 Db 7921 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 7980  
 QY 7981 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8040  
 Db 7981 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8040  
 QY 8041 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8100  
 Db 8041 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8100  
 QY 8101 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8160  
 Db 8101 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8160  
 QY 8161 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8220  
 Db 8161 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8220  
 QY 8221 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8280  
 Db 8221 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8280  
 QY 8281 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8340  
 Db 8281 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8340  
 QY 8341 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8400  
 Db 8341 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8400  
 QY 8401 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8460  
 Db 8401 NPTSEKPVLTHTPPNOMLYNNHSSSSNRSTGSGTSPDSHSS 8460

















GenCore version 5.1.4.D5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: April 23, 2003, 11:04:36 ; Search time 17 Seconds  
1133.263 alignments call updates/sec

Title: US-10-004-551-6

Sequence: 1 M1SANSFLITGKIGLFLD.....SSNSRSGSPDSHSES 649

Scoring table: RUSMG2 10, 0, Gapout 0.5

Searched: 262574 seqs. 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 04  
Maximum Match 1008  
Listing first 48 summaries

Database : Issued Patents\_Ah.\*  
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5: /cpn2.6/prodata/1/aa/5A.COM pep.\*  
6: /cpn2.6/prodata/1/aa/5A.COM pep.\*

Fold. No. is the number of results predicted by chance to have a  
score as high as the one being printed,  
and is derived by analysis of the total score distribution.

# SONARIES

Result	No.	Score	Match	length	DB	ID	Description
1	1284	96.6	619	4	US-09-188-910-325		Sequence 305, App
2	546	16.1	110	4	US-09-188-910-124		Sequence 2, Appl
3	375	11.7	708	4	US-09-131-684-2		Sequence 2, Appl
4	375	11.7	708	4	US-09-131-684-2		Sequence 2, Appl
5	334.5	10.4	673	4	US-09-063-950-2		Sequence 2, Appl
6	345.5	10.2	1480	4	US-09-182-0245-5		Sequence 5, Appl
7	345.5	10.2	1480	4	US-09-182-0245-5		Sequence 5, Appl
8	344.5	10.1	1480	4	US-09-540-245A-7		Sequence 7, Appl
9	344.5	10.1	1480	4	US-09-540-153-7		Sequence 7, Appl
10	344.5	10.1	1480	4	US-09-540-153-7		Sequence 7, Appl
11	344.5	10.1	1480	4	US-09-540-153-7		Sequence 7, Appl
12	343.5	10.1	1325	4	US-09-540-245A-2		Sequence 2, Appl
13	343.5	10.1	1325	4	US-09-540-245A-2		Sequence 2, Appl
14	342	10.1	282	1	US-08-42-053K-45		Sequence 45, Appl
15	342	10.1	322	1	US-08-42-053K-45		Sequence 45, Appl
16	342	10.1	333	1	US-08-42-063K-27		Sequence 27, Appl
17	342	10.1	342	1	US-08-772-919-2		Sequence 2, Appl
18	342	10.1	342	1	US-08-772-919-2		Sequence 2, Appl
19	342	10.1	342	1	US-08-42-063K-27		Sequence 27, Appl
20	342	10.1	359	1	US-08-103-218-4		Sequence 4, Appl
21	342	10.1	359	1	US-08-458-854-4		Sequence 4, Appl
22	335.5	9.9	375	4	US-08-188-634-1		Sequence 1, Appl
23	335.5	9.9	375	4	US-08-188-634-1		Sequence 1, Appl
24	333.5	9.8	375	1	US-08-103-218-2		Sequence 2, Appl
25	333.5	9.8	375	4	US-08-458-854-2		Sequence 2, Appl
26	333.5	9.8	375	4	US-08-458-854-2		Sequence 2, Appl
27	316.5	9.3	1091	3	US-08-465-485-5		Sequence 5, Appl

28 314.5 9.2 605 1 US-08-190-402A-49  
29 314.5 9.2 605 4 US-08-477-089-49  
30 314.5 9.2 605 4 US-08-477-089-49  
31 314.5 9.2 605 4 US-08-477-089-49  
32 311.5 9.2 605 4 US-09-063-200-5  
33 311.5 9.2 605 4 US-09-063-200-5  
34 306 9.0 603 4 US-08-477-446-50  
35 306 9.0 603 4 US-08-477-446-50  
36 306 9.0 603 4 US-08-477-089-50  
37 303 9.0 603 6 US-09-487-072A-50  
38 295.5 8.6 236 1 US-08-442-653A-42  
39 294 8.6 1101 3 US-08-386-485-2  
40 294 8.6 1101 3 US-08-386-485-2  
41 283.5 8.3 368 4 US-08-458-83A-3  
42 277.5 8.2 368 6 US-08-458-83A-3  
43 268.5 7.9 224 5 PCT-US91-09055-4  
44 268.5 7.9 224 5 PCT-US91-09055-4  
45 265.5 7.6 222 5 PCT-US91-09055-3

## ALIGNMENTS

RESULT 1  
US-05-188-930-305  
Sequence 305, Application US/0188930A  
Patent No. 5305500  
APPLICANT: Watson, James D.  
INVENTOR: Watson, James D.  
APPLICANT: Strachan, Lorna  
INVENTOR: Strachan, Lorna  
APPLICANT: Oursan, Rene  
INVENTOR: Oursan, Rene  
APPLICANT: Mulison, James Greg  
INVENTOR: Mulison, James Greg  
TITLE OF INVENTION: Compositions Isolated from Skin Cells  
AND METHODS OF USING THE SAME FOR THEIR USE  
FILE REFERENCE: 1100.1011C  
CURRENT APPLICATION NUMBER: US/09/188,930A  
CURRENT FILING DATE: 1998-11-09  
PCT NUMBER: 98/0188930A  
SOFTWARE: FASTSEQ FOR Windows Version 3.0  
SEQ ID NO 305  
LENGTH: 649  
ORGANISM: Mouse  
US-09-188-930-305

Query Match 96.6% Score 3284; DB 4; Length 649;  
Best Local Similarity 96.5% Pred No. 1.4e-267;  
Matches 626; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 M1SANSFLITGKIGLFLDWSVSCYCDAGTIGNDEITLPIGPIGDA 60  
DB 1 M1SANSFLITGKIGLFLDWSVSCYCDAGTIGNDEITLPIGPIGDA 60  
QY 61 TTTAQQNNGAGISDLKALVLELHNSLDEFTFPAVLELQENITLT 120  
DB 61 TTTAQQNNGAGISDLKALVLELHNSLDEFTFPAVLELQENITLT 120  
QY 121 YGSEKIPVLELALNNSAVFTEGAPQSKITVLELHNSLTPIGFPIEL 180  
DB 121 YGSEKIPVLELALNNSAVFTEGAPQSKITVLELHNSLTPIGFPIEL 180  
QY 181 RUDNDEITSSPQGLSEKLVLDGLHNNNGIGVFTFVNLTELVNLSAA 240  
DB 181 RUDNDEITSSPQGLSEKLVLDGLHNNNGIGVFTFVNLTELVNLSAA 240  
QY 241 PMLGQENKLVYQGHNVPFNPSFOLTEGDNHNNENFGIETLQITOL 300  
DB 241 PMLGQENKLVYQGHNVPFNPSFOLTEGDNHNNENFGIETLQITOL 300  
QY 301 TLRNPTGQCCWQVEMQLSPVNVNTELMQCFEVEGATLNNLFLPQDSRI 360  
DB 301 TLRNPTGQCCWQVEMQLSPVNVNTELMQCFEVEGATLNNLFLPQDSRI 360





PATENT NO. 622085  
GENERAL INFORMATION: CLASS A  
TITLE OF INVENTION: NOVEL LIGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF  
TITLE OF INVENTION: NOVEL LIGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF  
TITLE OF INVENTION: THEREFOR  
CURRENT APPLICATION NUMBER: US/09/063,950C  
CURRENT FILING DATE: 1998-04-21  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 673  
SEQ ID NO 674  
TYPE: PRT  
SOURCE: Homo sapiens  
US-09-063,950A  
US-09-063,950B

Query Match	10.4%	Score 354.5	DB #	Length 673
Best Local Similarity	24.5%	Prod. No. 38-23		
Matches 156	Conservative 101	Mismatches 261	Indels 119	Gaps 26
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100	Y	1	Y	1

RESULT 6  
US-09-182-024A-5  
Sequence 5, Application US/09182024A

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: GENERAL INFORMATION:
:
: APPLICANT: Connolly, Timothy
:
: APPLICANT: Rajput, Bhanu
:
: TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding

```







[illegible]

APPLICANT: CARBONS, JOSE  
APPLICANT: CRAIG, WILLIAM  
APPLICANT: MILLER, DAVID C.  
APPLICANT: MILLER, DAVID C.  
TITLE OF INVENTION: IMITATING CELL REGULATORY FACTORS  
NUMBER OF SEQUENCES: 62  
NUMBER OF AMINO ACIDS: 100  
NUMBER OF NUCLEOTIDES: 100  
ADDRESS: CARBONS AND FLORES  
CONDEMNATION, CARBONS AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122  
COMPUTER READABLE FORM: disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION NUMBER: 01/00000000, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/442,063A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 3510-0000  
PRECISE APPLICATION DATA:  
APPLICATION NUMBER: US 07/865,652  
FILING DATE: 03-APR-1992  
ATTORNEY: CARBONS, JOSE  
NAME: COMBELL, CATHERIN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/JOCHEK NUMBER: P-LA 1454  
TELEPHONE: 619-535-8001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE LENGTH: 232 amino acids

ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHERIN A.  
REGISTRATION NUMBER: 31-815  
REFERENCE/POCKET NUMBER: P-LA 1454  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids



GenCore version 5.1.4.m5.4578  
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OM protein - protein search, using sw model

Run on: April 23, 2003, 11:06:26 ; Search time 22 Seconds  
Maximum DB seq length: 2343825  
Maximum DB alignment cell updates/sec: 2343825

Title score: US-10-004-551-6

Sequence: 1 MISAANSLFLCTGLTGLTFA.....SSNSRDSFSPDSNHS 649

Scoring table: H405962 0, Gapart 0.5

Searched: 301932 seqs, 80139803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum match 100%

Listing first 40 summaries

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14: /usr98\_NMR\_PDB pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	3400	100.0	649	9	US-10-063-547-132	Sequence 132, App
2	3400	100.0	649	9	US-10-004-551-6	Sequence 6, Appl 1
3	3400	100.0	649	9	US-10-076-758-384	Sequence 384, App
4	3400	100.0	649	9	US-10-076-758-384	Sequence 384, App
5	3400	100.0	649	9	US-10-063-516-132	Sequence 132, App
6	3400	100.0	649	9	US-10-076-758-384	Sequence 384, App
7	3400	100.0	649	9	US-10-076-758-384	Sequence 384, App
8	3400	100.0	649	9	US-10-076-758-384	Sequence 384, App
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19	3400	100.0	649	9	US-10-076-758-384	Sequence 384, App

20 3400 100.0 649 9 US-10-174-589-384  
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45 3400 100.0 649 9 US-10-174-589-384

## ALIGNMENTS

RESULT 1  
US-10-063-547-132  
Sequence 132, Application US/10063547  
US-10-004-551-6  
Sequence 6, Appl 1

GENERAL INFORMATION: US/10063547

APPLICANT: Baton, Dan L.

APPLICANT: Fildoroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey

Handwritten signature/initials

US-10-063-547-132  
Sequence 132, Application US/10063547  
US-10-004-551-6  
Sequence 6, Appl 1

GENERAL INFORMATION: US/10063547

APPLICANT: Baton, Dan L.

APPLICANT: Fildoroff, Ellen

APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey

US-10-063-547-132  
Sequence 132, Application US/10063547  
US-10-004-551-6  
Sequence 6, Appl 1

GENERAL INFORMATION: US/10063547

APPLICANT: Baton, Dan L.

APPLICANT: Fildoroff, Ellen

APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

US-10-063-547-132  
Sequence 132, Application US/10063547  
US-10-004-551-6  
Sequence 6, Appl 1

GENERAL INFORMATION: US/10063547

APPLICANT: Baton, Dan L.

APPLICANT: Fildoroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

US-10-063-547-132  
Sequence 132, Application US/10063547  
US-10-004-551-6  
Sequence 6, Appl 1

GENERAL INFORMATION: US/10063547

APPLICANT: Baton, Dan L.

APPLICANT: Fildoroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

QY 181 RLDNRSTISPSGSGTSLKRLVLDNLNGLDQVFNVLNLTSLVNSIZAA 240  
 Db 181 RLDNRSTISPSGSGTSLKRLVLDNLNGLDQVFNVLNLTSLVNSIZAA 240  
 QY 241 PNLQVNTLRLKLTLDNLTNNVPPNPAVSTLQVTLPLDNNNNLSNLPQITDNLITOL 300  
 Db 241 PNLQVNTLRLKLTLDNLTNNVPPNPAVSTLQVTLPLDNNNNLSNLPQITDNLITOL 300  
 QY 301 ILRNPVYVCCCKMKNVWVKNLQSLPVPVYVGLQCAPEVYVGNVQALAPKPCDSOI 360  
 Db 301 ILRNPVYVCCCKMKNVWVKNLQSLPVPVYVGLQCAPEVYVGNVQALAPKPCDSOI 360  
 QY 361 VSTQITLITLNTVYVPAQGNWVPAVQDPIKHPKLDQVQTSKRTITVYVSTY 420  
 Db 361 VSTQITLITLNTVYVPAQGNWVPAVQDPIKHPKLDQVQTSKRTITVYVSTY 420  
 QY 421 DTIHSKLTALPMLSLKALHSPAGSTVTVGSRSKTLITVYVSTY 480  
 Db 421 DTIHSKLTALPMLSLKALHSPAGSTVTVGSRSKTLITVYVSTY 480  
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 Db 481 PMSLSNLTLPFTVETALALQVNTPTTLNRRDEKPTKNNPLAALIGAVLY 540  
 QY 541 TIALALVNVVHNSGLFNSKASGRRKDYTAGKTKNSLITFETSPMLPS 600  
 Db 541 TIALALVNVVHNSGLFNSKASGRRKDYTAGKTKNSLITFETSPMLPS 600  
 QY 601 NPTLSKEEPTVITLPPNGLNLTNNHSSSSNSTSGTISDUSHS 649  
 Db 601 NPTLSKEEPTVITLPPNGLNLTNNHSSSSNSTSGTISDUSHS 649

RESULT 2  
 US-10-004-551-6  
 : Sequence 6, Application US/1004551  
 : Patent Application No. US00004310A1  
 : GENERAL INFORMATION:  
 : APPLICANT: FERNANDEZ, RICHARD A.  
 : INVENTOR: FERNANDEZ, RICHARD A.  
 : FILE REFERENCE: 15966-559  
 : CURRENT APPLICATION NUMBER: US/10/004,551  
 : CURRENT FILING DATE: 2000-02-05  
 : PRIOR FILING DATE: 2000-08-10  
 : NUMBER OF SEQ ID NOS: 10  
 : NUMBER OF SEQ ID NOS: 10  
 : SEQ ID NO 6 Patent Ver. 2.1  
 : LENGTH: 649  
 : TYPE: PRT Homo sapiens  
 US-10-004-551-6

Query Match 100.0%; Score 3400; Db 9; Length 649;  
 Similarity 100.0%; Gaps 0;  
 Matches 649; Conservative 0; Mismatches 0;  
 QY 1 MTSANSTPLTGKIGLQVPLVSWKSCVYCDNAGTICNDPSTIPGPEDA 60  
 Db 1 MTSANSTPLTGKIGLQVPLVSWKSCVYCDNAGTICNDPSTIPGPEDA 60  
 QY 61 TLTALQNNWAGTIPDLAKVLTLYVNSLPPNPKYVVEHJDNENRPTT 120  
 Db 61 TLTALQNNWAGTIPDLAKVLTLYVNSLPPNPKYVVEHJDNENRPTT 120  
 QY 121 YNSSTPLTLEEHLQDVSANVSEIAPGNCYKLLRGLNSHTGTCW 180  
 Db 121 YNSSTPLTLEEHLQDVSANVSEIAPGNCYKLLRGLNSHTGTCW 180  
 QY 181 RLDNRSTISPSGSGTSLKRLVLDNLNGLDQVFNVLNLTSLVNSIZAA 240

Db 181 RLDNRSTISPSGSGTSLKRLVLDNLNGLDQVFNVLNLTSLVNSIZAA 240  
 QY 241 PNLQVNTLRLKLTLDNLTNNVPPNPAVSTLQVTLPLDNNNNLSNLPQITDNLITOL 300  
 Db 241 PNLQVNTLRLKLTLDNLTNNVPPNPAVSTLQVTLPLDNNNNLSNLPQITDNLITOL 300  
 QY 301 ILRNPVYVCCCKMKNVWVKNLQSLPVPVYVGLQCAPEVYVGNVQALAPKPCDSOI 360  
 Db 301 ILRNPVYVCCCKMKNVWVKNLQSLPVPVYVGLQCAPEVYVGNVQALAPKPCDSOI 360  
 QY 361 VSTQITLITLNTVYVPAQGNWVPAVQDPIKHPKLDQVQTSKRTITVYVSTY 420  
 Db 361 VSTQITLITLNTVYVPAQGNWVPAVQDPIKHPKLDQVQTSKRTITVYVSTY 420  
 QY 421 DTIHSKLTALPMLSLKALHSPAGSTVTVGSRSKTLITVYVSTY 480  
 Db 421 DTIHSKLTALPMLSLKALHSPAGSTVTVGSRSKTLITVYVSTY 480  
 QY 481 PMSLSNLTLPFTVETALALQVNTPTTLNRRDEKPTKNNPLAALIGAVLY 540  
 Db 481 PMSLSNLTLPFTVETALALQVNTPTTLNRRDEKPTKNNPLAALIGAVLY 540  
 QY 541 TIALALVNVVHNSGLFNSKASGRRKDYTAGKTKNSLITFETSPMLPS 600  
 Db 541 TIALALVNVVHNSGLFNSKASGRRKDYTAGKTKNSLITFETSPMLPS 600  
 QY 601 NPTLSKEEPTVITLPPNGLNLTNNHSSSSNSTSGTISDUSHS 649  
 Db 601 NPTLSKEEPTVITLPPNGLNLTNNHSSSSNSTSGTISDUSHS 649

RESULT 3  
 US-10-174-590-384  
 : Sequence 384, Application US/10174590  
 : Patent Application No. US00000352A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Baker, Kevin P.  
 : INVENTOR: Baker, Kevin P.  
 : APPLICANT: Chen, Jian  
 : INVENTOR: Chen, Jian  
 : APPLICANT: Goddard, Audrey  
 : INVENTOR: Goddard, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : INVENTOR: Godowski, Paul J.  
 : APPLICANT: Rudey, Austin L.  
 : INVENTOR: Rudey, Austin L.  
 : APPLICANT: Smith, Victoria  
 : INVENTOR: Smith, Victoria  
 : APPLICANT: Switaba, Colin K.  
 : INVENTOR: Switaba, Colin K.  
 : APPLICANT: Zhang, Zemin  
 : INVENTOR: Zhang, Zemin  
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 : ACIDS  
 : FILE OF INVENTION: ACIDS ENCODING THE SAME  
 : CURRENT APPLICATION NUMBER: US/10/174,590  
 : CURRENT FILING DATE: 2002-06-18  
 : PRIOR FILING DATE: 2002-06-18  
 : NUMBER OF SEQ ID NOS: 612  
 : NUMBER OF SEQ ID NOS: 612  
 : SEQ ID NO 384  
 : LENGTH: 649  
 : TYPE: PRT Homo sapiens  
 US-10-174-590-384

Query Match 100.0%; Score 1400; Db 9; Length 649;  
 Similarity 100.0%; Gaps 0;  
 Matches 649; Conservative 0; Mismatches 0;  
 QY 1 MTSANSTPLTGKIGLQVPLVSWKSCVYCDNAGTICNDPSTIPGPEDA 60  
 Db 1 MTSANSTPLTGKIGLQVPLVSWKSCVYCDNAGTICNDPSTIPGPEDA 60  
 QY 61 TLTALQNNWAGTIPDLAKVLTLYVNSLPPNPKYVVEHJDNENRPTT 120  
 Db 61 TLTALQNNWAGTIPDLAKVLTLYVNSLPPNPKYVVEHJDNENRPTT 120  
 QY 121 YNSSTPLTLEEHLQDVSANVSEIAPGNCYKLLRGLNSHTGTCW 180  
 Db 121 YNSSTPLTLEEHLQDVSANVSEIAPGNCYKLLRGLNSHTGTCW 180  
 QY 181 RLDNRSTISPSGSGTSLKRLVLDNLNGLDQVFNVLNLTSLVNSIZAA 240



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Db 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Db 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Qy 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Qy 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Db 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Qy 241 PVLNPTNLSKLTADNHNVPNPNSTLQITLFDJNSNNSNLSNLSIPMLPRTIEL 300
Qy 241 PVLNPTNLSKLTADNHNVPNPNSTLQITLFDJNSNNSNLSNLSIPMLPRTIEL 300
Qy 301 TLNRSPTCCOCHWNTKQSLPYKVNWGLCAKAPKPNVAKANLPCVCSGI 360
Qy 301 TLNRSPTCCOCHWNTKQSLPYKVNWGLCAKAPKPNVAKANLPCVCSGI 360
Db 301 TLNRSPTCCOCHWNTKQSLPYKVNWGLCAKAPKPNVAKANLPCVCSGI 360
Qy 361 VSTQITLAPNVPVAGQWAPVQPDQKMFALQDQGTGSRKTTITVMSYS 420
Qy 361 VSTQITLAPNVPVAGQWAPVQPDQKMFALQDQGTGSRKTTITVMSYS 420
Db 361 VSTQITLAPNVPVAGQWAPVQPDQKMFALQDQGTGSRKTTITVMSYS 420
Qy 421 DTHHSKLAHPALHLSKLGHSRAPSSTITVYGBRSSTVLPALPSPFYKQV 480
Qy 421 DTHHSKLAHPALHLSKLGHSRAPSSTITVYGBRSSTVLPALPSPFYKQV 480
Db 421 DTHHSKLAHPALHLSKLGHSRAPSSTITVYGBRSSTVLPALPSPFYKQV 480
Qy 481 PMFSNLTFLPFWCTETAPLNKNTTFLARSEKSTVLPALPSPFYKQV 540
Qy 481 PMFSNLTFLPFWCTETAPLNKNTTFLARSEKSTVLPALPSPFYKQV 540
Db 481 PMFSNLTFLPFWCTETAPLNKNTTFLARSEKSTVLPALPSPFYKQV 540
Qy 541 TALLAUVNVRHNSLSRNCASGRKRDYAPAGTKNSLFRFETFWMLPS 600
Qy 541 TALLAUVNVRHNSLSRNCASGRKRDYAPAGTKNSLFRFETFWMLPS 600
Db 541 TALLAUVNVRHNSLSRNCASGRKRDYAPAGTKNSLFRFETFWMLPS 600
Qy 601 NPISEKSVITHTFPFNNKLTNNSSSSNSSTGSDGSDUSHS 649
Qy 601 NPISEKSVITHTFPFNNKLTNNSSSSNSSTGSDGSDUSHS 649
Db 601 NPISEKSVITHTFPFNNKLTNNSSSSNSSTGSDGSDUSHS 649

RESULT 6
; Sequence 384, Application US/10176758
; Publication No. US20030008353AL
; GENPAT INFORMATION:
; APPLICANT: Chem. Jisan P.
; APPLICANT: Desrochers, Luc
; APPLICANT: Godek, Paul J.
; APPLICANT: Godek, Paul J.
; APPLICANT: Gurey, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Rasmussen, Maria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P430R1C104 US 01/076758
; CURRENT FILING DATE: 2002-05-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; TYPE: PRT
; LENGTH: 649
; ORGANISM: Homo Sapien
US-10-176-758-384
Query Match 100.0%; Score 3400; DB 9; Length 649;
Best Local Similarity 100.0%; Pred. No. 3,3e-261;
Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MISANSLTFLGTLGLZAVASVNAKSCFVCKDAGFYCNHRTISIPGIZEDA 60
Db 1 MISANSLTFLGTLGLZAVASVNAKSCFVCKDAGFYCNHRTISIPGIZEDA 60

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Qy 61 TTXLQNNVNNATPQVAKLAVERTITFNSLDEPNTVYKLYVLSYVNSATA 120
Db 61 TTXLQNNVNNATPQVAKLAVERTITFNSLDEPNTVYKLYVLSYVNSATA 120
Qy 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 121 YDSLSKPTFLSELDJNSVANSIESRPFNSLTLELSNLSNLSIPMLPRTIEL 180
Qy 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Qy 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Db 181 KIDNRSITSSLSGLTSKLYLQORLANNESLKNVYKLYVLSYVNSATA 240
Qy 241 PVLNPTNLSKLTADNHNVPNPNSTLQITLFDJNSNNSNLSNLSIPMLPRTIEL 300
Qy 241 PVLNPTNLSKLTADNHNVPNPNSTLQITLFDJNSNNSNLSNLSIPMLPRTIEL 300
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Qy 301 TLNRSPTCCOCHWNTKQSLPYKVNWGLCAKAPKPNVAKANLPCVCSGI 360
Db 301 TLNRSPTCCOCHWNTKQSLPYKVNWGLCAKAPKPNVAKANLPCVCSGI 360
Qy 361 VSTQITLAPNVPVAGQWAPVQPDQKMFALQDQGTGSRKTTITVMSYS 420
Qy 361 VSTQITLAPNVPVAGQWAPVQPDQKMFALQDQGTGSRKTTITVMSYS 420
Db 361 VSTQITLAPNVPVAGQWAPVQPDQKMFALQDQGTGSRKTTITVMSYS 420
Qy 421 DTHHSKLAHPALHLSKLGHSRAPSSTITVYGBRSSTVLPALPSPFYKQV 480
Qy 421 DTHHSKLAHPALHLSKLGHSRAPSSTITVYGBRSSTVLPALPSPFYKQV 480
Db 421 DTHHSKLAHPALHLSKLGHSRAPSSTITVYGBRSSTVLPALPSPFYKQV 480
Qy 481 PMFSNLTFLPFWCTETAPLNKNTTFLARSEKSTVLPALPSPFYKQV 540
Qy 481 PMFSNLTFLPFWCTETAPLNKNTTFLARSEKSTVLPALPSPFYKQV 540
Db 481 PMFSNLTFLPFWCTETAPLNKNTTFLARSEKSTVLPALPSPFYKQV 540
Qy 541 TALLAUVNVRHNSLSRNCASGRKRDYAPAGTKNSLFRFETFWMLPS 600
Qy 541 TALLAUVNVRHNSLSRNCASGRKRDYAPAGTKNSLFRFETFWMLPS 600
Db 541 TALLAUVNVRHNSLSRNCASGRKRDYAPAGTKNSLFRFETFWMLPS 600
Qy 601 NPISEKSVITHTFPFNNKLTNNSSSSNSSTGSDGSDUSHS 649
Qy 601 NPISEKSVITHTFPFNNKLTNNSSSSNSSTGSDGSDUSHS 649
Db 601 NPISEKSVITHTFPFNNKLTNNSSSSNSSTGSDGSDUSHS 649

RESULT 5
US-10-063-616-132
; Sequence 132, Application US/10063616
; Publication No. US20030013855AL
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvercoff, Ellen
; APPLICANT: Godek, Paul J.
; APPLICANT: Godek, Paul J.
; APPLICANT: Godek, Paul J.
; APPLICANT: Grimsald, Christopher J.
; APPLICANT: Grimsald, Christopher J.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P323OR1C1
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; TYPE: PRT
; LENGTH: 649
; ORGANISM: Homo Sapien
US-10-063-616-132
Query Match 100.0%; Score 3400; DB 9; Length 649;
Best Local Similarity 100.0%; Pred. No. 3,3e-261;
Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MISANSLTFLGTLGLZAVASVNAKSCFVCKDAGFYCNHRTISIPGIZEDA 60
Qy 1 MISANSLTFLGTLGLZAVASVNAKSCFVCKDAGFYCNHRTISIPGIZEDA 60

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Db 61 TITLONNINNAIPDSKALUKVITERTISDEPPLKPTVKEHLQNNIRIT 120
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Db 121 YGSEATPWEHLKNSVANSIPEAPYKLELFLSNNLSTPMLPTTEL 180
QY 181 RUDNRSSTSSQGLSEKALVLDONNINNAIYNSGKQVFWKLSVNSLTA 240
Db 181 RUDNRSSTSSQGLSEKALVLDONNINNAIYNSGKQVFWKLSVNSLTA 240
QY 241 PNLQTNLKLITLQNNINNVPPNASTLAQLRDMSNNLSLQPTDQDNLQTL 300
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QY 301 ILNNPPTCCKMKNVWGLASLKYVWVGLQACAPKPVKALDULNRFPCDSGI 360
Db 301 ILNNPPTCCKMKNVWGLASLKYVWVGLQACAPKPVKALDULNRFPCDSGI 360
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Db 361 VSTQITTAINTVYPAQOWAPVTKPDKNPKLDOQGTGSPSKRTITVSTYS 420
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Db 421 DTHLSKMLAPALSLKLGSPAGSITETVGERSELVTALEPSPKVM 480
QY 481 PMSNLTLFDETPCIEETAPLKNPTTARBEKEPKYNPLPALIGAVLY 540
Db 481 PMSNLTLFDETPCIEETAPLKNPTTARBEKEPKYNPLPALIGAVLY 540
QY 541 TALLAUKVYVHNSLSFNKCAKSKRRKDYABGKNSLLEIETSPULPIS 600
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QY 601 NEPIKEKEEHTIPPNNKMLKNNSSESSNUSSTGSGIPDSHES 649
Db 601 NEPIKEKEEHTIPPNNKMLKNNSSESSNUSSTGSGIPDSHES 649

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## RESULT 6

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US-10-174-737-384
; Sequence 384, Application US/10175737
; Publication No. US20030013153AL
; GENERAL INFORMATION
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desdoyere, Luc
; APPLICANT: Gosselin, Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurey, Austin L.
; APPLICANT: Hach, Charles
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F439LC50
; CURRENT FILING DATE: 2002-06-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; LENGTH: 649
; TYPE: PRT
US-10-174-737-384

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Query Match Similarity 100.00; Score 3400; Ins 9; Length 649;
Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MISANSITLGTGKIGLJFJAVPLSWANSPCYCHMGACHTGACNFTISPTGIPDA 60
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Db 61 TITLONNINNAIPDSKALUKVITERTISDEPPLKPTVKEHLQNNIRIT 120
QY 121 YGSEATPWEHLKNSVANSIPEAPYKLELFLSNNLSTPMLPTTEL 180
Db 121 YGSEATPWEHLKNSVANSIPEAPYKLELFLSNNLSTPMLPTTEL 180
QY 181 RUDNRSSTSSQGLSEKALVLDONNINNAIYNSGKQVFWKLSVNSLTA 240
Db 181 RUDNRSSTSSQGLSEKALVLDONNINNAIYNSGKQVFWKLSVNSLTA 240
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QY 301 ILNNPPTCCKMKNVWGLASLKYVWVGLQACAPKPVKALDULNRFPCDSGI 360
Db 301 ILNNPPTCCKMKNVWGLASLKYVWVGLQACAPKPVKALDULNRFPCDSGI 360
QY 361 VSTQITTAINTVYPAQOWAPVTKPDKNPKLDOQGTGSPSKRTITVSTYS 420
Db 361 VSTQITTAINTVYPAQOWAPVTKPDKNPKLDOQGTGSPSKRTITVSTYS 420
QY 421 DTHLSKMLAPALSLKLGSPAGSITETVGERSELVTALEPSPKVM 480
Db 421 DTHLSKMLAPALSLKLGSPAGSITETVGERSELVTALEPSPKVM 480
QY 481 PMSNLTLFDETPCIEETAPLKNPTTARBEKEPKYNPLPALIGAVLY 540
Db 481 PMSNLTLFDETPCIEETAPLKNPTTARBEKEPKYNPLPALIGAVLY 540
QY 541 TALLAUKVYVHNSLSFNKCAKSKRRKDYABGKNSLLEIETSPULPIS 600
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QY 601 NEPIKEKEEHTIPPNNKMLKNNSSESSNUSSTGSGIPDSHES 649
Db 601 NEPIKEKEEHTIPPNNKMLKNNSSESSNUSSTGSGIPDSHES 649

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## RESULT 7

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US-10-063-502-132
; Sequence 132, Application US/10063502
; Publication No. US20030023042AL
; GENERAL INFORMATION
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvetoff, Ellen
; APPLICANT: Gosselin, Paul J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Katsch, David B.
; APPLICANT: Matarazzo, John
; APPLICANT: Matarazzo, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; PRIORITY DATE: 2002-05-01
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; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 132
; LENGTH: 649
; TYPE: PRT

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/ TITLE OF INVENTION: SECRETED AND TRANSDERNAME POLYPEPTIDES AND NUCLEIC  
 / FILE REFERENCE: P430R04G45  
 / CURRENT APPLICATION NUMBER: US/10/175-738  
 / CURRENT FILING DATE: 2002-06-19  
 / NUMBER OF SEQ ID NOS: 612  
 / SEQ ID NO 384  
 / TYPE: PRT  
 / ORGANISM: Homo Sapien  
 / US-10-175-738-384

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/ Sequence 384, Application US/1017572  
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/ APPLICANT: Baker, Kevin P.  
 / APPLICANT: Chen, Jian

/ APPLICANT: Demoyers, Luc  
 / APPLICANT: Gossard, Paul

/ APPLICANT: Gurney, Austin L.  
 / APPLICANT:

/ APPLICANT: Pat, James  
 / APPLICANT: Smith, Alexander  
 / APPLICANT: Metcalf, Colin K.  
 / APPLICANT: Wood, William K.  
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 / TITLE OF INVENTION: SECRETED AND TRANSDERNAME POLYPEPTIDES AND NUCLEIC  
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/ Sequence 384, Application US/10176482  
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/ APPLICANT: Baker, Kevin P.  
 / APPLICANT:













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[illegible]



[illegible][illegible]

Wed Apr 23 13:51:21 2003

us-10-004-551-6.rpr

Page 9

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Job time : 26 secs

















[illegible][illegible]











SEQUENCE FROM N.A.  
 RP TSPDSE-PROTEOLYCAN: PubMed=10644529;  
 RC Wu M.X., Zhang O., Umno N., Darke J.B., Nathanielsz P.W.;  
 BA "Characterization of decalin mRNA in pregnant intrauterine tissues of  
 BT the sheep and goat." *Am J Reprod Med* 57(1):105-110 (2003).  
 BT M.D. 97, PubMed=12781397-0206(2003).  
 CC -1- FUNCTION: May affect the rate of fibrils formation (By  
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 CC -1- TSP-beta. Binds to type I and type II collagen, to fibronectin and  
 CC TSP-beta. Forms a ternary complex with MMP2 and ELM (By  
 CC similarity).  
 CC -1- PRO-1. Extracellular matrix (By similarity).  
 CC -1- PRO-2. The attached glycosaminoglycan chain can be either  
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue  
 CC of origin (By similarity).  
 CC -1- PRO-3. SMALL LECTINE-RICH PROTEOLYCAN  
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 12 LECTINE-RICH REPEATS (LRR).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use, but the EMBL outstation - the European Bioinformatics Institute  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/annouce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: AF125041; AAE00585.1;  
 CC HSP: P09661.1A9N.  
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 CC InterPro: IPRO03582; LRR\_Out.  
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